

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Tryggvason, Karl
Kallunki, Pekka
Pyke, Charles

(ii) TITLE OF INVENTION: Laminin Chains: Diagnostic Uses

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fay Sharpe Fagan Minnich & McKee
(B) STREET: 1100 Superior Ave, Suite 700
(C) CITY: Cleveland
(D) STATE: Ohio
(E) COUNTRY: USA
(F) ZIP: 44114

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unknown
(B) FILING DATE: 08 January 2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/663,147
(B) FILING DATE: 150-September 2000
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Minnich, Richard, J.
(B) REGISTRATION NUMBER: 24,175
(C) REFERENCE/DOCKET NUMBER: TRV 20014

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 216-861-5582
(B) TELEFAX: 216-241-1666

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTCACCAA GACTTACACA

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATCACTGA GCAGCTGAAC

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGTACCAGA ACCGAGTTCG

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGTTACCA GGCTTGAGAG

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTACTGCGGA ATCTCACAGC

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACACTGTTC AACCCAGGGT

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAACAAGCCC TCTCACTGGT

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGGAGACTG TGCTGATAAG

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATACCTCTC TACATGGCAT

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGTCTCGCTG AATCTCTCTT

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTACAAC TAG CATGGTGCCC

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 118..183

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 118..3699

(ix) FEATURE:

- (A) NAME/KEY: polyA_site
- (B) LOCATION: 4433

(ix) FEATURE:

- (A) NAME/KEY: polyA_site
- (B) LOCATION: 5195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCACCTGA TCGAAGGAAA AGGAAGGCAC AGCGGAGCGC AGAGTGAGAA CCACCAACCG	60
AGGCGCCGGG CAGCGACCCC TGCAGCGGAG ACAGAGACTG AGCGGCCCGG CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu 1 5 10 15	165
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly 20 25 30	213
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly 35 40 45	261
AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His 50 55 60	309
TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg 65 70 75 80	357
TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys 85 90 95	405
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg 100 105 110	453
TGC GAC CGA TGT CTG CCA GGC TTC CAC ATG CTC ACG GAT GCG GGG TGC Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys 115 120 125	501
ACC CAA GAC CAG AGA CTG CTA GAC TCC AAG TGT GAC TGT GAC CCA GCT Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala 130 135 140	549
GGC ATC GCA GGG CCC TGT GAC GCG GGC CGC TGT GTC TGC AAG CCA GCT Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala 145 150 155 160	597
GTT ACT GGA GAA CGC TGT GAT AGG TGT CGA TCA GGT TAC TAT AAT CTG Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu 165 170 175	645
GAT GGG GGG AAC CCT GAG GGC TGT ACC CAG TGT TTC TGC TAT GGG CAT Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His 180 185 190	693
TCA GCC AGC TGC CGC AGC TCT GCA GAA TAC AGT GTC CAT AAG ATC ACC Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr 195 200 205	741
TCT ACC TTT CAT CAA GAT GTT GAT GGC TGG AAG GCT GTC CAA CGA AAT Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn	789

תוצאות חישוב קידוד גנטי
 של סדרת הנתונים
 הנתונה למעלה

210		215		220		
GGG TCT CCT GCA AAG CTC CAA TGG TCA CAG CGC CAT CAA GAT GTG TTT	837					
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe						
225 230 235 240						
AGC TCA GCC CAA CGA CTA GAT CCT GTC TAT TTT GTG GCT CCT GCC AAA	885					
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys						
245 250 255						
TTT CTT GGG AAT CAA CAG GTG AGC TAT GGG CAA AGC CTG TCC TTT GAC	933					
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp						
260 265 270						
TAC CGT GTG GAC AGA GGA GGC AGA CAC CCA TCT GCC CAT GAT GTG ATC	981					
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile						
275 280 285						
CTG GAA GGT GCT GGT CTA CGG ATC ACA GCT CCC TTG ATG CCA CTT GGC	1029					
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly						
290 295 300						
AAG ACA CTG CCT TGT GGG CTC ACC AAG ACT TAC ACA TTC AGG TTA AAT	1077					
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn						
305 310 315 320						
GAG CAT CCA AGC AAT AAT TGG AGC CCC CAG CTG AGT TAC TTT GAG TAT	1125					
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr						
325 330 335						
CGA AGG TTA CTG CGG AAT CTC ACA GCC CTC CGC ATC CGA GCT ACA TAT	1173					
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr						
340 345 350						
GGA GAA TAC AGT ACT GGG TAC ATT GAC AAT GTG ACC CTG ATT TCA GCC	1221					
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala						
355 360 365						
CGC CCT GTC TCT GGA GCC CCA GCA CCC TGG GTT GAA CAG TGT ATA TGT	1269					
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys						
370 375 380						
CCT GTT GGG TAC AAG GGG CAA TTC TGC CAG GAT TGT GCT TCT GGC TAC	1317					
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr						
385 390 395 400						
AAG AGA GAT TCA GCG AGA CTG GGG CCT TTT GGC ACC TGT ATT CCT TGT	1365					
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys						
405 410 415						
AAC TGT CAA GGG GGA GGG GCC TGT GAT CCA GAC ACA GGA GAT TGT TAT	1413					
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr						
420 425 430						
TCA GGG GAT GAG AAT CCT GAC ATT GAG TGT GCT GAC TGC CCA ATT GGT	1461					
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly						
435 440 445						
TTC TAC AAC GAT CCG CAC GAC CCC CGC AGC TGC AAG CCA TGT CCC TGT	1509					

AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA	2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg	
690 695 700	
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC	2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His	
705 710 715 720	
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC	2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser	
725 730 735	
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT	2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn	
740 745 750	
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC	2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His	
755 760 765	
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC	2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp	
770 775 780	
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA	2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly	
785 790 795 800	
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT	2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu	
805 810 815	
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG	2613
Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg	
820 825 830	
GAG GCC ACT CAA GCG GAA ATT GAA GCA GAT AGG TCT TAT CAG CAC AGT	2661
Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser	
835 840 845	
CTC CGC CTC CTG GAT TCA GTG TCT CCG CTT CAG GGA GTC AGT GAT CAG	2709
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln	
850 855 860	
TCC TTT CAG GTG GAA GAA GCA AAG AGG ATC AAA CAA AAA GCG GAT TCA	2757
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser	
865 870 875 880	
CTC TCA AGC CTG GTA ACC AGG CAT ATG GAT GAG TTC AAG CGT ACA CAA	2805
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln	
885 890 895	
AAG AAT CTG GGA AAC TGG AAA GAA GAA GCA CAG CAG CTC TTA CAG AAT	2853
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn	
900 905 910	
GGA AAA AGT GGG AGA GAG AAA TCA GAT CAG CTG CTT TCC CGT GCC AAT	2901
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn	

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CTT GCT AAA AGC AGA GCA CAA GAA GCA CTG AGT ATG GGC AAT GCC ACT Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr 930 935 940			2949
TTT TAT GAA GTT GAG AGC ATC CTT AAA AAC CTC AGA GAG TTT GAC CTG Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu 945 950 955 960			2997
CAG GTG GAC AAC AGA AAA GCA GAA GCT GAA GAA GCC ATG AAG AGA CTC Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu 965 970 975			3045
TCC TAC ATC AGC CAG AAG GTT TCA GAT GCC AGT GAC AAG ACC CAG CAA Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln 980 985 990			3093
GCA GAA AGA GCC CTG GGG AGC GCT GCT GCT GAT GCA CAG AGG GCA AAG Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys 995 1000 1005			3141
AAT GGG GCC GGG GAG GCC CTG GAA ATC TCC AGT GAG ATT GAA CAG GAG Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu 1010 1015 1020			3189
ATT GGG AGT CTG AAC TTG GAA GCC AAT GTG ACA GCA GAT GGA GCC TTG Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu 1025 1030 1035 1040			3237
GCC ATG GAA AAG GGA CTG GCC TCT CTG AAG AGT GAG ATG AGG GAA GTG Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val 1045 1050 1055			3285
GAA GGA GAG CTG GAA AGG AAG GAG CTG GAG TTT GAC ACG AAT ATG GAT Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp 1060 1065 1070			3333
GCA GTA CAG ATG GTG ATT ACA GAA GCC CAG AAG GTT GAT ACC AGA GCC Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala 1075 1080 1085			3381
AAG AAC GCT GGG GTT ACA ATC CAA GAC ACA CTC AAC ACA TTA GAC GGC Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly 1090 1095 1100			3429
CTC CTG CAT CTG ATG GAC CAG CCT CTC AGT GTA GAT GAA GAG GGG CTG Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu 1105 1110 1115 1120			3477
GTC TTA CTG GAG CAG AAG CTT TCC CGA GCC AAG ACC CAG ATC AAC AGC Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser 1125 1130 1135			3525
CAA CTG CGG CCC ATG ATG TCA GAG CTG GAA GAG AGG GCA CGT CAG CAG Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln 1140 1145 1150			3573

AGG GGC CAC CTC CAT TTG CTG GAG ACA AGC ATA GAT GGG ATT CTG GCT	3621
Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala	
1155 1160 1165	
GAT GTG AAG AAC TTG GAG AAC ATT AGG GAC AAC CTG CCC CCA GGC TGC	3669
Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys	
1170 1175 1180	
TAC AAT ACC CAG GCT CTT GAG CAA CAG TGA AGCTGCCATA AATATTTCTC	3719
Tyr Asn Thr Gln Ala Leu Glu Gln Gln *	
1185 1190	
AACTGAGGTT CTTGGGATAC AGATCTCAGG GCTCGGGAGC CATGTCATGT GAGTGGGTGG	3779
GATGGGGACA TTTGAACATG TTTAATGGGT ATGCTCAGGT CAACTGACCT GACCCCATTC	3839
CTGATCCCAT GGCCAGGTGG TTGTCTTATT GCACCATACT CCTTGCTTCC TGATGCTGGG	3899
CATGAGGCAG ATAGGCACTG GTGTGAGAAT GATCAAGGAT CTGGACCCCA AAGATAGACT	3959
GGATGGAAAG ACAAACTGCA CAGGCAGATG TTTGCCTCAT AATAGTCGTA AGTGGAGTCC	4019
TGGAATTTGG ACAAGTGCTG TTGGGATATA GTCAACTTAT TCTTTGAGTA ATGTGACTAA	4079
AGGAAAAAAC TTTGACTTTG CCCAGGCATG AAATTCTTCC TAATGTCAGA ACAGAGTGCA	4139
ACCCAGTCAC ACTGTGGCCA GTAAAATACT ATTGCCTCAT ATTGTCCTCT GCAAGCTTCT	4199
TGCTGATCAG AGTTCCTCCT ACTTACAACC CAGGGTGTGA ACATGTTCTC CATTTTCAAG	4259
CTGGAAGAAG TGAGCAGTGT TGGAGTGAGG ACCTGTAAGG CAGGCCCATC CAGAGCTATG	4319
GTGCTTGCTG GTGCCTGCCA CCTTCAAGTT CTGGACCTGG GCATGACATC CTTTCTTTTA	4379
ATGATGCCAT GGCAACTTAG AGATTGCATT TTTATTAAAG CATTTCTTAC CAGCAAAGCA	4439
AATGTTGGGA AAGTATTTAC TTTTTCGGTT TCAAAGTGAT AGAAAAGTGT GGCTTGGGCA	4499
TTGAAAGAGG TAAAATTCTC TAGATTTATT AGTCCTAATT CAATCCTACT TTTCGAACAC	4559
CAAAAATGAT GCGCATCAAT GTATTTTATC TTATTTTCTC AATCTCCTCT CTCTTTCTCT	4619
CACCCATAAT AAGAGAATGT TCCTACTCAC ACTTCAGCTG GGTCACATCC ATCCCTCCAT	4679
TCATCCTTCC ATCCATCTTT CCATCCATTA CCTCCATCCA TCCTTCCAAC ATATATTTAT	4739
TGAGTACCTA CTGTGTGCCA GGGGCTGGTG GGACAGTGGT GACATAGTCT CTGCCCTCAT	4799
AGAGTTGATT GTCTAGTGAG GAAGACAAGC ATTTTTAAAA AATAAATTTA AACTTACAAA	4859
CTTTGTTTGT CACAAGTGGT GTTTATTGCA ATAACCGCTT GGTTTGCAAC CTCTTTGCTC	4919
AACAGAACAT ATGTTGCAAG ACCCTCCCAT GGGCACTGAG TTTGGCAAGG ATGACAGAGC	4979
TCTGGGTTGT GCACATTTCT TTGCATTCCA GCGTCACTCT GTGCCTTCTA CAACTGATTG	5039
CAACAGACTG TTGAGTTATG ATAACACCAG TGGGAATTGC TGGAGGAACC AGAGGCACTT	5099
CCACCTTGGC TGGGAAGACT ATGGTGCTGC CTTGCTTCTG TATTTCTTCTG GATTTTCCTG	5159

1155 1160 1165
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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
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Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
 20             25             30

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
 35             40             45

Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
 50             55             60

Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
 65             70             75             80

Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
 85             90             95

Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
100             105             110

Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
115             120             125

Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130             135             140

Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145             150             155             160

Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
165             170             175

Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180             185             190

Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
195             200             205

Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210             215             220

Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225             230             235             240

Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys

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	565		570		575
Pro Met Gly	Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val				
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Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser					
	595		600		605
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met					
	610		615		620
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly					
	625		630		635
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala					
	645		650		655
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly					
	660		665		670
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu					
	675		680		685
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg					
	690		695		700
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His					
	705		710		715
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser					
	725		730		735
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn					
	740		745		750
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His					
	755		760		765
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp					
	770		775		780
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly					
	785		790		795
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu					
	805		810		815
Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg					
	820		825		830
Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser					
	835		840		845
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln					
	850		855		860
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser					
	865		870		875
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln					

				885				890				895			
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn
			900				905						910		
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn
			915				920						925		
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr
			930				935						940		
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu
			945				950						955		
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu
			965							970			975		
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln
			980				985						990		
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys
			995				1000						1005		
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu
			1010				1015						1020		
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu
			1025				1030						1035		
Ala	Met	Glu	Lys	Gly	Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val
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Glu	Gly	Glu	Leu	Glu	Arg	Lys	Glu	Leu	Glu	Phe	Asp	Thr	Asn	Met	Asp
			1060							1065			1070		
Ala	Val	Gln	Met	Val	Ile	Thr	Glu	Ala	Gln	Lys	Val	Asp	Thr	Arg	Ala
			1075				1080						1085		
Lys	Asn	Ala	Gly	Val	Thr	Ile	Gln	Asp	Thr	Leu	Asn	Thr	Leu	Asp	Gly
			1090				1095						1100		
Leu	Leu	His	Leu	Met	Asp	Gln	Pro	Leu	Ser	Val	Asp	Glu	Glu	Gly	Leu
			1105				1110						1115		
Val	Leu	Leu	Glu	Gln	Lys	Leu	Ser	Arg	Ala	Lys	Thr	Gln	Ile	Asn	Ser
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Gln	Leu	Arg	Pro	Met	Met	Ser	Glu	Leu	Glu	Glu	Arg	Ala	Arg	Gln	Gln
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			1155				1160						1165		
Asp	Val	Lys	Asn	Leu	Glu	Asn	Ile	Arg	Asp	Asn	Leu	Pro	Pro	Gly	Cys
			1170				1175						1180		
Tyr	Asn	Thr	Gln	Ala	Leu	Glu	Gln	Gln	*						
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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 118..183

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 118..3453

- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 4021..4316
 - (D) OTHER INFORMATION: /rpt_type= "other"
- /rpt_family= "HUMAN ALU"

- (ix) FEATURE:
 - (A) NAME/KEY: polyA_site
 - (B) LOCATION: 4296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACCACCTGA TCGAAGGAAA AGGAAGGCAC AGCGGAGCGC AGAGTGAGAA CCACCAACCG	60
AGGCGCCGGG CAGCGACCCC TGCAGCGGAG ACAGAGACTG AGCGGCCCGG CACCGCC	117
ATG CCT GCG CTC TGG CTG GGC TGC TGC CTC TGC TTC TCG CTC CTC CTG	165
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu	
1195 1200 1205 1210	
CCC GCA GCC CGG GCC ACC TCC AGG AGG GAA GTC TGT GAT TGC AAT GGG	213
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly	
1215 1220 1225	
AAG TCC AGG CAG TGT ATC TTT GAT CGG GAA CTT CAC AGA CAA ACT GGT	261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly	
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AAT GGA TTC CGC TGC CTC AAC TGC AAT GAC AAC ACT GAT GGC ATT CAC	309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His	
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TGC GAG AAG TGC AAG AAT GGC TTT TAC CGG CAC AGA GAA AGG GAC CGC	357
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg	
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TGT TTG CCC TGC AAT TGT AAC TCC AAA GGT TCT CTT AGT GCT CGA TGT	405
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys	
1275 1280 1285 1290	
GAC AAC TCT GGA CGG TGC AGC TGT AAA CCA GGT GTG ACA GGA GCC AGA	453

Asp	Asn	Ser	Gly	Arg	Cys	Ser	Cys	Lys	Pro	Gly	Val	Thr	Gly	Ala	Arg	
				1295					1300					1305		
TGC	GAC	CGA	TGT	CTG	CCA	GGC	TTC	CAC	ATG	CTC	ACG	GAT	GCG	GGG	TGC	501
Cys	Asp	Arg	Cys	Leu	Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys	
			1310					1315					1320			
ACC	CAA	GAC	CAG	AGA	CTG	CTA	GAC	TCC	AAG	TGT	GAC	TGT	GAC	CCA	GCT	549
Thr	Gln	Asp	Gln	Arg	Leu	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala	
			1325				1330					1335				
GGC	ATC	GCA	GGG	CCC	TGT	GAC	GCG	GGC	CGC	TGT	GTC	TGC	AAG	CCA	GCT	597
Gly	Ile	Ala	Gly	Pro	Cys	Asp	Ala	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala	
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GTT	ACT	GGA	GAA	CGC	TGT	GAT	AGG	TGT	CGA	TCA	GGT	TAC	TAT	AAT	CTG	645
Val	Thr	Gly	Glu	Arg	Cys	Asp	Arg	Cys	Arg	Ser	Gly	Tyr	Tyr	Asn	Leu	
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GAT	GGG	GGG	AAC	CCT	GAG	GGC	TGT	ACC	CAG	TGT	TTC	TGC	TAT	GGG	CAT	693
Asp	Gly	Gly	Asn	Pro	Glu	Gly	Cys	Thr	Gln	Cys	Phe	Cys	Tyr	Gly	His	
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TCA	GCC	AGC	TGC	CGC	AGC	TCT	GCA	GAA	TAC	AGT	GTC	CAT	AAG	ATC	ACC	741
Ser	Ala	Ser	Cys	Arg	Ser	Ser	Ala	Glu	Tyr	Ser	Val	His	Lys	Ile	Thr	
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TCT	ACC	TTT	CAT	CAA	GAT	GTT	GAT	GGC	TGG	AAG	GCT	GTC	CAA	CGA	AAT	789
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GGG	TCT	CCT	GCA	AAG	CTC	CAA	TGG	TCA	CAG	CGC	CAT	CAA	GAT	GTG	TTT	837
Gly	Ser	Pro	Ala	Lys	Leu	Gln	Trp	Ser	Gln	Arg	His	Gln	Asp	Val	Phe	
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Ser	Ser	Ala	Gln	Arg	Leu	Asp	Pro	Val	Tyr	Phe	Val	Ala	Pro	Ala	Lys	
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TTT	CTT	GGG	AAT	CAA	CAG	GTG	AGC	TAT	GGG	CAA	AGC	CTG	TCC	TTT	GAC	933
Phe	Leu	Gly	Asn	Gln	Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp	
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Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	His	Pro	Ser	Ala	His	Asp	Val	Ile	
			1470				1475						1480			
CTG	GAA	GGT	GCT	GGT	CTA	CGG	ATC	ACA	GCT	CCC	TTG	ATG	CCA	CTT	GGC	1029
Leu	Glu	Gly	Ala	Gly	Leu	Arg	Ile	Thr	Ala	Pro	Leu	Met	Pro	Leu	Gly	
		1485				1490				1495						
AAG	ACA	CTG	CCT	TGT	GGG	CTC	ACC	AAG	ACT	TAC	ACA	TTC	AGG	TTA	AAT	1077
Lys	Thr	Leu	Pro	Cys	Gly	Leu	Thr	Lys	Thr	Tyr	Thr	Phe	Arg	Leu	Asn	
	1500					1505				1510						
GAG	CAT	CCA	AGC	AAT	AAT	TGG	AGC	CCC	CAG	CTG	AGT	TAC	TTT	GAG	TAT	1125
Glu	His	Pro	Ser	Asn	Asn	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu	Tyr	
1515					1520				1525						1530	
CGA	AGG	TTA	CTG	CGG	AAT	CTC	ACA	GCC	CTC	CGC	ATC	CGA	GCT	ACA	TAT	1173

1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530

Arg	Arg	Leu	Leu	Arg	Asn	Leu	Thr	Ala	Leu	Arg	Ile	Arg	Ala	Thr	Tyr	
				1535					1540					1545		
GGA	GAA	TAC	AGT	ACT	GGG	TAC	ATT	GAC	AAT	GTG	ACC	CTG	ATT	TCA	GCC	1221
Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Ile	Ser	Ala	
			1550					1555					1560			
CGC	CCT	GTC	TCT	GGA	GCC	CCA	GCA	CCC	TGG	GTT	GAA	CAG	TGT	ATA	TGT	1269
Arg	Pro	Val	Ser	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Gln	Cys	Ile	Cys	
		1565					1570					1575				
CCT	GTT	GGG	TAC	AAG	GGG	CAA	TTC	TGC	CAG	GAT	TGT	GCT	TCT	GGC	TAC	1317
Pro	Val	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Asp	Cys	Ala	Ser	Gly	Tyr	
	1580					1585				1590						
AAG	AGA	GAT	TCA	GCG	AGA	CTG	GGG	CCT	TTT	GGC	ACC	TGT	ATT	CCT	TGT	1365
Lys	Arg	Asp	Ser	Ala	Arg	Leu	Gly	Pro	Phe	Gly	Thr	Cys	Ile	Pro	Cys	
1595					1600					1605					1610	
AAC	TGT	CAA	GGG	GGA	GGG	GCC	TGT	GAT	CCA	GAC	ACA	GGA	GAT	TGT	TAT	1413
Asn	Cys	Gln	Gly	Gly	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Tyr	
			1615					1620					1625			
TCA	GGG	GAT	GAG	AAT	CCT	GAC	ATT	GAG	TGT	GCT	GAC	TGC	CCA	ATT	GGT	1461
Ser	Gly	Asp	Glu	Asn	Pro	Asp	Ile	Glu	Cys	Ala	Asp	Cys	Pro	Ile	Gly	
			1630					1635					1640			
TTC	TAC	AAC	GAT	CCG	CAC	GAC	CCC	CGC	AGC	TGC	AAG	CCA	TGT	CCC	TGT	1509
Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys	
		1645					1650					1655				
CAT	AAC	GGG	TTC	AGC	TGC	TCA	GTG	ATT	CCG	GAG	ACG	GAG	GAG	GTG	GTG	1557
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Ile	Pro	Glu	Thr	Glu	Glu	Val	Val	
	1660					1665				1670						
TGC	AAT	AAC	TGC	CCT	CCC	GGG	GTC	ACC	GGT	GCC	CGC	TGT	GAG	CTC	TGT	1605
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys	
1675				1680				1685						1690		
GCT	GAT	GGC	TAC	TTT	GGG	GAC	CCC	TTT	GGT	GAA	CAT	GGC	CCA	GTG	AGG	1653
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg	
			1695					1700					1705			
CCT	TGT	CAG	CCC	TGT	CAA	TGC	AAC	AGC	AAT	GTG	GAC	CCC	AGT	GCC	TCT	1701
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Ser	Asn	Val	Asp	Pro	Ser	Ala	Ser	
		1710						1715					1720			
GGG	AAT	TGT	GAC	CGG	CTG	ACA	GGC	AGG	TGT	TTG	AAG	TGT	ATC	CAC	AAC	1749
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn	
		1725					1730					1735				
ACA	GCC	GGC	ATC	TAC	TGC	GAC	CAG	TGC	AAA	GCA	GGC	TAC	TTC	GGG	GAC	1797
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp	
	1740					1745					1750					
CCA	TTG	GCT	CCC	AAC	CCA	GCA	GAC	AAG	TGT	CGA	GCT	TGC	AAC	TGT	AAC	1845
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn	
1755				1760				1765						1770		
CCC	ATG	GGC	TCA	GAG	CCT	GTA	GGA	TGT	CGA	AGT	GAT	GGC	ACC	TGT	GTT	1893

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val	
1775 1780 1785	
TGC AAG CCA GGA TTT GGT GGC CCC AAC TGT GAG CAT GGA GCA TTC AGC	1941
Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser	
1790 1795 1800	
TGT CCA GCT TGC TAT AAT CAA GTG AAG ATT CAG ATG GAT CAG TTT ATG	1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met	
1805 1810 1815	
CAG CAG CTT CAG AGA ATG GAG GCC CTG ATT TCA AAG GCT CAG GGT GGT	2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly	
1820 1825 1830	
GAT GGA GTA GTA CCT GAT ACA GAG CTG GAA GGC AGG ATG CAG CAG GCT	2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala	
1835 1840 1845 1850	
GAG CAG GCC CTT CAG GAC ATT CTG AGA GAT GCC CAG ATT TCA GAA GGT	2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly	
1855 1860 1865	
GCT AGC AGA TCC CTT GGT CTC CAG TTG GCC AAG GTG AGG AGC CAA GAG	2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu	
1870 1875 1880	
AAC AGC TAC CAG AGC CGC CTG GAT GAC CTC AAG ATG ACT GTG GAA AGA	2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg	
1885 1890 1895	
GTT CGG GCT CTG GGA AGT CAG TAC CAG AAC CGA GTT CGG GAT ACT CAC	2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His	
1900 1905 1910	
AGG CTC ATC ACT CAG ATG CAG CTG AGC CTG GCA GAA AGT GAA GCT TCC	2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser	
1915 1920 1925 1930	
TTG GGA AAC ACT AAC ATT CCT GCC TCA GAC CAC TAC GTG GGG CCA AAT	2373
Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn	
1935 1940 1945	
GGC TTT AAA AGT CTG GCT CAG GAG GCC ACA AGA TTA GCA GAA AGC CAC	2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His	
1950 1955 1960	
GTT GAG TCA GCC AGT AAC ATG GAG CAA CTG ACA AGG GAA ACT GAG GAC	2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp	
1965 1970 1975	
TAT TCC AAA CAA GCC CTC TCA CTG GTG CGC AAG GCC CTG CAT GAA GGA	2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly	
1980 1985 1990	
GTC GGA AGC GGA AGC GGT AGC CCG GAC GGT GCT GTG GTG CAA GGG CTT	2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu	
1995 2000 2005 2010	
GTG GAA AAA TTG GAG AAA ACC AAG TCC CTG GCC CAG CAG TTG ACA AGG	2613

1941 1989 2037 2085 2133 2181 2229 2277 2325 2373 2421 2469 2517 2565 2613
 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 2000 2005 2010

Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg		
2015									2020			2025					
GAG	GCC	ACT	CAA	GCG	GAA	ATT	GAA	GCA	GAT	AGG	TCT	TAT	CAG	CAC	AGT	2661	
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser		
2030									2035			2040					
CTC	CGC	CTC	CTG	GAT	TCA	GTG	TCT	CCG	CTT	CAG	GGA	GTC	AGT	GAT	CAG	2709	
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Pro	Leu	Gln	Gly	Val	Ser	Asp	Gln		
2045									2050			2055					
TCC	TTT	CAG	GTG	GAA	GAA	GCA	AAG	AGG	ATC	AAA	CAA	AAA	GCG	GAT	TCA	2757	
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser		
2060									2065			2070					
CTC	TCA	AGC	CTG	GTA	ACC	AGG	CAT	ATG	GAT	GAG	TTC	AAG	CGT	ACA	CAA	2805	
Leu	Ser	Ser	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln		
2075									2080			2085				2090	
AAG	AAT	CTG	GGA	AAC	TGG	AAA	GAA	GAA	GCA	CAG	CAG	CTC	TTA	CAG	AAT	2853	
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn		
2095									2100			2105					
GGA	AAA	AGT	GGG	AGA	GAG	AAA	TCA	GAT	CAG	CTG	CTT	TCC	CGT	GCC	AAT	2901	
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn		
2110									2115			2120					
CTT	GCT	AAA	AGC	AGA	GCA	CAA	GAA	GCA	CTG	AGT	ATG	GGC	AAT	GCC	ACT	2949	
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr		
2125									2130			2135					
TTT	TAT	GAA	GTT	GAG	AGC	ATC	CTT	AAA	AAC	CTC	AGA	GAG	TTT	GAC	CTG	2997	
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu		
2140									2145			2150					
CAG	GTG	GAC	AAC	AGA	AAA	GCA	GAA	GCT	GAA	GAA	GCC	ATG	AAG	AGA	CTC	3045	
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu		
2155									2160			2165				2170	
TCC	TAC	ATC	AGC	CAG	AAG	GTT	TCA	GAT	GCC	AGT	GAC	AAG	ACC	CAG	CAA	3093	
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln		
2175									2180			2185					
GCA	GAA	AGA	GCC	CTG	GGG	AGC	GCT	GCT	GCT	GAT	GCA	CAG	AGG	GCA	AAG	3141	
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys		
2190									2195			2200					
AAT	GGG	GCC	GGG	GAG	GCC	CTG	GAA	ATC	TCC	AGT	GAG	ATT	GAA	CAG	GAG	3189	
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu		
2205									2210			2215					
ATT	GGG	AGT	CTG	AAC	TTG	GAA	GCC	AAT	GTG	ACA	GCA	GAT	GGA	GCC	TTG	3237	
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu		
2220									2225			2230					
GCC	ATG	GAA	AAG	GGA	CTG	GCC	TCT	CTG	AAG	AGT	GAG	ATG	AGG	GAA	GTG	3285	
Ala	Met	Glu	Lys	Gly	Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val		
2235									2240			2245				2250	
GAA	GGA	GAG	CTG	GAA	AGG	AAG	GAG	CTG	GAG	TTT	GAC	ACG	AAT	ATG	GAT	3333	

100%
 90%
 80%
 70%
 60%
 50%
 40%
 30%
 20%
 10%
 0%

Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp	
2255	2260 2265
GCA GTA CAG ATG GTG ATT ACA GAA GCC CAG AAG GTT GAT ACC AGA GCC	3381
Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala	
2270	2275 2280
AAG AAC GCT GGG GTT ACA ATC CAA GAC ACA CTC AAC ACA TTA GAC GGC	3429
Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly	
2285	2290 2295
CTC CTG CAT CTG ATG GGT ATG TGA ACCCACAACC CACAACCTTC CAGCTCCATG	3483
Leu Leu His Leu Met Gly Met *	
2300	2305
CTCCAGGGCT TTGCTCCAGA ACACTCACTA TACCTAGCCC CAGCAAAGGG GAGTCTCAGC	3543
TTTCCTTAAG GATATCAGTA AATGTGCTTT GTTTCCAGGC CCAGATAACT TTCGGCAGGT	3603
TCCCTTACAT TTA CTG GACC CTGTTTACC GTTGCTAAGA TGGGTCACCTG AACACCTATT	3663
GCACTTGGGG GTAAAGGTCT GTGGGCCAAA GAACAGGTGT ATATAAGCAA CTTACAGAA	3723
CACGAGACAG CTTGGGAATC CTGCTAAAGA GTCTGGCCTG GACCCTGAGA AGCCAGTGGA	3783
CAGTTTTAAG CAGAGGAATA ACATCACCAC TGTATATTTC AGAAAGATCA CTAGGGCAGC	3843
CGAGTGGAGG AAAGCTTGAA GAGGGGGTTA GAGAGAAGGC AGGTTGAGAC TACTTAAGAT	3903
ATTGTTGAAA TAATTGAAGA GAGAAATGAC AGGAGCCTGC TCTAAGGCAG TAGAATGGTG	3963
GCTGGGAAGA TGTGAAGGAA GATTTTCCCA GTCTGTGAAG TCAAGAATCA CTTGCCGGCC	4023
GGGTGTGGTG GCTCACGCCT GTAATTCTAG CACTTTGGGA GACTGAAGCG GGTGGATCAC	4083
CCGAGGTCAG GAGTTGAAGA CCAGCCTGGC CAACATGGTG AAACCCTGTC TCTACTAAAA	4143
GTACAAAAAT TAGCTGGATG ATGGTGGTGG GCGCCTGTAA TTCCAGCTAC TCAGGAGTCT	4203
GAGGCAGGAG AATCGCTTGA ACCCAGGAGG CGAGGTTACA GTGAGCCAAG ATTGCACCAC	4263
TGCTCTTCCA GCCTGGGAAC AGAGAGACTG CCTAAAAAAA AAAAAAAAAA AAA	4316

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu	
1	5 10 15
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly	
20	25 30

Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
 35 40 45
 Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
 50 55 60
 Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
 65 70 75 80
 Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
 85 90 95
 Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
 100 105 110
 Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
 115 120 125
 Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
 130 135 140
 Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
 145 150 155 160
 Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
 165 170 175
 Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
 180 185 190
 Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
 195 200 205
 Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
 210 215 220
 Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
 225 230 235 240
 Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
 245 250 255
 Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
 260 265 270
 Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
 275 280 285
 Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
 290 295 300
 Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
 305 310 315 320
 Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
 325 330 335
 Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
 340 345 350

Gly 355	Glu 355	Tyr 355	Ser 355	Thr 355	Gly 355	Tyr 355	Ile 360	Asp 360	Asn 360	Val 360	Thr 365	Leu 365	Ile 365	Ser 365	Ala 365
Arg 370	Pro 370	Val 370	Ser 370	Gly 370	Ala 370	Pro 375	Ala 375	Pro 375	Trp 375	Val 380	Glu 380	Gln 380	Cys 380	Ile 380	Cys 380
Pro 385	Val 385	Gly 385	Tyr 385	Lys 385	Gly 390	Gln 390	Phe 390	Cys 390	Gln 395	Asp 395	Cys 395	Ala 395	Ser 395	Gly 400	Tyr 400
Lys 405	Arg 405	Asp 405	Ser 405	Ala 405	Arg 405	Leu 405	Gly 410	Pro 410	Phe 410	Gly 410	Thr 410	Cys 410	Ile 410	Pro 415	Cys 415
Asn 420	Cys 420	Gln 420	Gly 420	Gly 420	Gly 420	Ala 420	Cys 425	Asp 425	Pro 425	Asp 425	Thr 425	Gly 430	Asp 430	Cys 430	Tyr 430
Ser 435	Gly 435	Asp 435	Glu 435	Asn 435	Pro 435	Asp 440	Ile 440	Glu 440	Cys 440	Ala 440	Asp 445	Cys 445	Pro 445	Ile 445	Gly 445
Phe 450	Tyr 450	Asn 450	Asp 450	Pro 450	His 450	Asp 455	Pro 455	Arg 455	Ser 455	Cys 455	Lys 460	Pro 460	Cys 460	Pro 460	Cys 460
His 465	Asn 465	Gly 465	Phe 465	Ser 465	Cys 470	Ser 470	Val 470	Ile 470	Pro 470	Glu 475	Thr 475	Glu 475	Glu 475	Val 480	Val 480
Cys 485	Asn 485	Asn 485	Cys 485	Pro 485	Pro 485	Gly 485	Val 485	Thr 485	Gly 490	Ala 490	Arg 490	Cys 490	Glu 490	Leu 495	Cys 495
Ala 500	Asp 500	Gly 500	Tyr 500	Phe 500	Gly 500	Asp 500	Pro 505	Phe 505	Gly 505	Glu 505	His 505	Gly 510	Pro 510	Val 510	Arg 510
Pro 515	Cys 515	Gln 515	Pro 515	Cys 515	Gln 515	Cys 515	Asn 520	Ser 520	Asn 520	Val 520	Asp 520	Pro 525	Ser 525	Ala 525	Ser 525
Gly 530	Asn 530	Cys 530	Asp 530	Arg 530	Leu 530	Thr 535	Gly 535	Arg 535	Cys 535	Leu 535	Lys 540	Cys 540	Ile 540	His 540	Asn 540
Thr 545	Ala 545	Gly 545	Ile 545	Tyr 545	Cys 550	Asp 550	Gln 550	Cys 550	Lys 550	Ala 555	Gly 555	Tyr 555	Phe 555	Gly 560	Asp 560
Pro 565	Leu 565	Ala 565	Pro 565	Asn 565	Pro 565	Ala 565	Asp 565	Lys 565	Cys 570	Arg 570	Ala 570	Cys 570	Asn 575	Cys 575	Asn 575
Pro 580	Met 580	Gly 580	Ser 580	Glu 580	Pro 580	Val 580	Gly 585	Cys 585	Arg 585	Ser 585	Asp 585	Gly 590	Thr 590	Cys 590	Val 590
Cys 595	Lys 595	Pro 595	Gly 595	Phe 595	Gly 595	Gly 595	Pro 600	Asn 600	Cys 600	Glu 600	His 600	Gly 605	Ala 605	Phe 605	Ser 605
Cys 610	Pro 610	Ala 610	Cys 610	Tyr 610	Asn 610	Gln 615	Val 615	Lys 615	Ile 615	Gln 615	Met 620	Asp 620	Gln 620	Phe 620	Met 620
Gln 625	Gln 625	Leu 625	Gln 625	Arg 625	Met 630	Glu 630	Ala 630	Leu 630	Ile 630	Ser 635	Lys 635	Ala 635	Gln 635	Gly 640	Gly 640
Asp 645	Gly 645	Val 645	Val 645	Pro 645	Asp 645	Thr 645	Glu 645	Leu 645	Glu 650	Gly 650	Arg 650	Met 650	Gln 650	Gln 655	Ala 655
Glu 660	Gln 660	Ala 660	Leu 660	Gln 660	Asp 660	Ile 660	Leu 665	Arg 665	Asp 665	Ala 665	Gln 665	Ile 665	Ser 670	Glu 670	Gly 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
900 905 910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln Glu
1010 1015 1020

Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu
1025 1030 1035 1040

Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val
1045 1050 1055

Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp
1060 1065 1070

Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala
1075 1080 1085

Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly
1090 1095 1100

Leu Leu His Leu Met Gly Met *

1105 1110

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCGCAGAG TGAGAACCAC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligomer primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGTATTCT GCAGAGCTGC

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligomer primers"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCCTTTCCCCTACCTTGTG

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGAAGCCTGGCAGACAT

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "OLIGOMER PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Gly Thr Cys Thr Thr Thr Ala Thr Ala Gly Gly Gly Ala Gly Gly
1 5 10 15
Thr Thr Gly Gly Cys Cys Ala Gly Thr Cys Ala Ala Thr Ala Gly Gly
20 25 30
Thr Thr Ala Cys Thr Thr Thr Ala Thr Gly Ala Gly Thr Thr Gly Cys
35 40 45
Thr Ala Ala Cys Cys Cys Thr Gly Gly Thr Gly Ala Gly Cys Ala Gly
50 55 60
Gly Ala Ala Gly Thr Thr Ala Thr Gly Thr Gly Gly Ala Cys Cys Ala
65 70 75 80
Gly Gly Ala Gly Ala Gly Ala Ala Ala Cys Cys Cys Thr Thr Gly Gly

Thr Thr Cys Ala Gly Cys Cys Thr Gly Gly Ala Gly Ala Ala Ala Gly
 100 105 110
 Gly Ala Gly Ala Gly Gly Thr Thr Gly Ala Cys Cys Cys Thr Ala Ala
 115 120 125
 Ala Cys Thr Gly Gly Ala Gly Gly Gly Thr Gly Gly Ala Gly Ala Gly
 130 135 140
 Gly Ala Cys Cys Cys Thr Gly Thr Thr Gly Thr Gly Ala Cys Thr Cys
 145 150 155 160
 Thr Cys Cys Gly Ala Cys Thr Gly Ala Cys Thr Thr Gly Thr Cys Thr
 165 170 175
 Thr Cys Cys Thr Thr Gly Ala Thr Gly Thr Cys Cys Thr Thr Thr Ala
 180 185 190
 Ala Gly Cys Cys Gly Gly Ala Gly Cys Thr Gly Ala Thr Thr Cys Gly
 195 200 205
 Gly Gly Cys Thr Gly Cys Thr Gly Cys Cys Thr Thr Ala Thr Thr Thr
 210 215 220
 Cys Thr Gly Ala Gly Thr Thr Ala Gly Cys Gly Cys Thr Cys Thr Thr
 225 230 235 240
 Ala Ala Gly Ala Thr Thr Gly Gly Gly Cys Cys Thr Cys Cys Cys Ala
 245 250 255
 Gly Thr Thr Thr Gly Ala Gly Gly Ala Ala Gly Gly Gly Cys Gly
 260 265 270
 Gly Gly Cys Thr Gly Cys Thr Gly Thr Cys Thr Ala Cys Cys Thr Cys
 275 280 285
 Thr Gly Thr Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
 290 295 300
 Ala Cys Cys Ala Cys Cys Cys Cys Gly Gly Gly Ala Gly Ala Gly Ala
 305 310 315 320
 Ala Gly Gly Ala Gly Gly Gly Cys Thr Cys Cys Gly Gly Gly Gly Ala
 325 330 335
 Ala Thr Cys Thr Cys Gly Cys Ala Cys Ala Thr Thr Cys Cys Ala Gly
 340 345 350
 Gly Cys Ala Ala Ala Gly Gly Cys Thr Cys Cys Cys Gly Gly Gly Cys
 355 360 365
 Cys Gly Cys Ala Gly Cys Cys Thr Cys Thr Gly Thr Gly Cys Cys Ala
 370 375 380
 Cys Ala Cys Cys Cys Thr Thr Gly Gly Cys Cys Cys Gly Gly Gly Cys
 385 390 395 400
 Cys Ala Gly Gly Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Cys Cys

405

410

415

Thr Cys Gly Cys Thr Gly Cys Gly Ala Gly Gly Gly Gly Gly Ala Gly
420 425 430

Cys Gly Gly Gly Cys Gly Gly Cys Thr Gly Cys Gly Gly Gly Gly Ala
435 440 445

Gly Cys Gly Ala Thr Thr Thr Thr Cys Cys Ala Gly Cys Cys Cys Gly
450 455 460

Gly Thr Thr Thr Gly Thr Gly Cys Thr Cys Thr Gly Thr Gly Thr Gly
465 470 475 480

Thr Thr Thr Gly Thr Cys Thr Gly Cys Cys Thr Cys Thr Gly Gly Ala
485 490 495

Gly Gly Gly Cys Thr Gly Gly Gly Thr Cys Cys Thr Cys Cys Thr Thr
500 505 510

Ala Thr Thr Cys Ala Cys Ala Gly Gly Thr Gly Ala Gly Thr Cys Ala
515 520 525

Cys Ala Cys Cys Cys Thr Gly Ala Ala Ala Cys Ala Cys Ala Gly Gly
530 535 540

Cys Thr Cys Thr Cys Thr Thr Cys Cys Thr Gly Thr Cys Ala Gly Gly
545 550 555 560

Ala Cys Thr Gly Ala Gly Thr Cys Ala Gly Gly Thr Ala Gly Ala Ala
565 570 575

Gly Ala Gly Thr Cys Gly Ala Thr Ala Ala Ala Ala Cys Cys Ala Cys
580 585 590

Cys Thr Gly Ala Thr Cys Ala Ala Gly Gly Ala Ala Ala Ala Gly Gly
595 600 605

Ala Ala Gly Gly Cys Ala Cys Ala Gly Cys Gly Gly Ala Gly Cys Gly
610 615 620

Cys Ala Gly Ala Gly Thr Gly Ala Gly Ala Ala Cys Cys Ala Cys Cys
625 630 635 640

Ala Ala Cys Cys Gly Ala Gly Gly Cys Gly Cys Cys Gly Gly Gly Cys
645 650 655

Ala Gly Cys Gly Ala Cys Cys Cys Cys Thr Gly Cys Ala Gly Cys Gly
660 665 670

Gly Ala Gly Ala Cys Ala Gly Ala Gly Ala Cys Thr Gly Ala Gly Cys
675 680 685

Gly Gly Cys Cys Cys Gly Gly Cys Ala Cys Cys Gly Cys Cys Ala Thr
690 695 700

Gly Cys Cys Thr Gly Cys Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly
705 710 715 720